

## SEQUENCE LISTING

<110> Kere, Juha  
Taipale, Mikko  
Nopola-Hemmi, Jaana  
Kaminen, Nina

<120> Novel Human Gene Functionally Related To Dyslexia

<130> DYXC1

<140>

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<170> PatentIn Ver. 2.1

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<212> DNA  
<213> Homo sapiens

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<223> human DYXC1 mRNA as cDNA

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act gcg gtc ttt ctg tct ctg ccc ctc aaa ggc gtg tgc gtc aga gac 458  
Thr Ala Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp  
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acg gac gtg ttc tgc acg gaa aac tat ctg aag gtc aac ttt cct cca 506  
Thr Asp Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro  
35 40 45  
ttt tta ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc 554  
Phe Leu Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser  
50 55 60  
aaa gca aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa 602  
Lys Ala Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys  
65 70 75  
gaa gcg gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag 650  
Glu Ala Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu  
80 85 90  
atg atg caa aga att aga gaa aaa tct att tta caa gca caa gag aga 698  
Met Met Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg  
95 100 105 110  
gca aaa gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa 746  
Ala Lys Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln  
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Lys Tyr Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Arg Lys  
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aaa ata gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gca 842  
Lys Ile Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Ala  
145 150 155  
ttg gaa gcc tgg aaa gaa tat caa aga aaa gct gag gag caa aaa aaa 890  
Leu Glu Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys  
160 165 170  
att cag aga gaa gag aaa tta tgt caa aaa gaa aag caa att aaa gaa 938  
Ile Gln Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu

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aag tta aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att Lys Leu Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile				1082
225	230		235	
aaa atc aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca Lys Ile Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser				1130
240	245		250	
caa gta gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga Gln Val Ala Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg				1178
255	260		265	
270				
aga gca atg aat act gac ata gct gaa ctt tgc gat tta aaa gaa gaa Arg Ala Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu				1226
275	280		285	
gaa aag aac cca gaa tgg ttg aag gat aaa gga aac aaa ttg ttt gca Glu Lys Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala				1274
290	295		300	
acg gaa aac tat ttg gca gct atc aat gca tat aat tta gcc ata aga Thr Glu Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg				1322
305	310		315	
cta aat aat aag atg cca cta ttg tat ttg aac cgg gct gct tgc cac Leu Asn Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His				1370
320	325		330	
cta aaa cta aaa aac tta cac aag gct att gaa gat tct tct aag gca Leu Lys Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala				1418
335	340		345	
350				
ctg gaa tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg Leu Glu Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met				1466
355	360		365	
aag gca cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat Lys Ala His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr				1514
370	375		380	
385	390		395	
gta gaa ggc cta cag gat tat gaa gcg gca ctt aag att gat cca tcc Val Glu Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser				1562
400	405		410	
aac aaa att gta caa att gat gct gag aag att cgg aat gta att caa Asn Lys Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln				1610
415	420			
gga aca gaa cta aaa tct taatgactat tagaagtaac taagtattgt Gly Thr Glu Leu Lys Ser				1658
415	420			

tataagttt taaaaacaa ctggaggcat cttgtacat attatggcca gttgtacaga 1718  
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 <223> human DYXCI mRNA as cDNA

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 35 40 45  
 Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala  
 50 55 60  
 Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala  
 65 70 75 80  
 Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met  
 85 90 95  
 Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys  
 100 105 110  
 Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr  
 115 120 125  
 Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Arg Lys Lys Ile  
 130 135 140  
 Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Ala Leu Glu  
 145 150 155 160  
 Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln  
 165 170 175  
 Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Gly Arg  
 180 185 190  
 Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn  
 195 200 205  
 Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu

210	215	220
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile		
225	230	235
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val		
245	250	255
Ala Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala		
260	265	270
Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys		
275	280	285
Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu		
290	295	300
Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn		
305	310	315
320		
Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys		
325	330	335
Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu		
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Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala		
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His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu		
370	375	380
Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys		
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Glu Leu Lys Ser		
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Ser Leu Pro Leu Arg Gly Val Cys Val Arg Asp Ala Asp Val Phe Cys			
20	25	30	35
ggg gaa agt tac ctg aag gtt aac ttt cct cca ttt tta ttt gag ctg			200
Gly Glu Ser Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu Phe Glu Leu			
40	45	50	
t <sub>tt</sub> ctc tat gct ccc ata gat gat ggg aag agc aaa gcc aag att gga			248
Phe Leu Tyr Ala Pro Ile Asp Asp Gly Lys Ser Lys Ala Lys Ile Gly			
55	60	65	
aat gac acg att ctt ttc aca ttg tat aaa aag gag cca gtt ctg tgg			296
Asn Asp Thr Ile Leu Phe Thr Leu Tyr Lys Glu Pro Val Leu Trp			
70	75	80	
gat agc ctt tct gtg cc <sub>g</sub> ggt gtt gat aaa gag atg atg cag aga ata			344
Asp Ser Leu Ser Val Pro Gly Val Asp Lys Glu Met Met Gln Arg Ile			
85	90	95	
aga gaa aaa tct atc ttg caa gca cag gag aaa gca aaa gag gcc aca			392
Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Lys Ala Lys Glu Ala Thr			
100	105	110	115
gaa gca aaa gct gtt gcc aag cga gaa gac cag aga tac gca cta gg <sub>c</sub>			440
Glu Ala Lys Ala Val Ala Lys Arg Glu Asp Gln Arg Tyr Ala Leu Gly			
120	125	130	
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Glu Met Met Lys Ile Glu Glu Glu Arg Lys Lys Leu Glu Asp Leu			
135	140	145	
aaa gaa aat gaa cgg aaa aag gca act agc gaa tta gaa gcg tgg aaa			536
Lys Glu Asn Glu Arg Lys Lys Ala Thr Ser Glu Leu Glu Ala Trp Lys			
150	155	160	
gaa tgt caa aag aaa gct gac gga caa aaa aga gtc cag agg aag gag			584
Glu Cys Gln Lys Lys Ala Asp Gly Gln Lys Arg Val Gln Arg Lys Glu			
165	170	175	
aaa ccg ctc gag gga aag caa gct gaa gag acc aaa gct cta aaa cct			632
Lys Pro Leu Glu Gly Lys Gln Ala Glu Glu Thr Lys Ala Leu Lys Pro			
180	185	190	195
cg <sub>g</sub> ggt ttg ccc cg <sub>g</sub> aag gcc cca ccc act cgc ctc ccc aca aga gg <sub>g</sub>			680
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agg aat tgg gaa aac ata ttt cct gag aag tta aag gaa gac aga gtc			728
Arg Asn Trp Glu Asn Ile Phe Pro Glu Lys Leu Lys Glu Asp Arg Val			
215	220	225	
cct gcg cct cgc tcc gct gg <sub>c</sub> agt att caa atc agc ttt acc cct cga			776
Pro Ala Pro Arg Ser Ala Gly Ser Ile Gln Ile Ser Phe Thr Pro Arg			
230	235	240	
gtg ttc cca aca gca ctt cg <sub>g</sub> gaa tcc caa gtc gca gaa gag gag gag			824
Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val Ala Glu Glu Glu			

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tgg ctg cat aaa caa gca gaa gca cg <sup>g</sup> aga g <sup>c</sup> cc atg agc act gac ctt			872
Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala Met Ser Thr Asp Leu			
260	265	270	275
cct gag ttc ttt gac tta aaa gaa gaa gag agg aat cca gac tgg ttg			920
Pro Glu Phe Phe Asp Leu Lys Glu Glu Arg Asn Pro Asp Trp Leu			
280	285	290	
aaa gac aag gga aac aaa ttg ttt gca aca gaa aac tat ttg gca gc <sup>g</sup>			968
Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu Asn Tyr Leu Ala Ala			
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Val Asp Ala Tyr Asn Leu Ala Ile Arg Leu Asn Cys Lys Ile Pro Leu			
310	315	320	
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325	330	335	
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Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu Leu Leu Thr Pro Pro			
340	345	350	355
gtt gct gac aat gcc aat gca aga atg aag gca cac gtc cga cga ggg			1160
Val Ala Asp Asn Ala Asn Ala Arg Met Lys Ala His Val Arg Arg Gly			
360	365	370	
aca gc <sup>g</sup> ttc tgt caa cta gaa ttg tat gtt gaa ggc ttg caa gat tat			1208
Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu Gly Leu Gln Asp Tyr			
375	380	385	
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Glu Ala Ala Leu Lys Ile Asp Pro Ala Asn Thr Val Val Gln Asn Asp			
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Ala Glu Lys Ile Arg Asn Ile Ile Gln Gly Thr Ala Leu Lys Ser Arg			
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35 40 45  
Phe Glu Leu Phe Leu Tyr Ala Pro Ile Asp Asp Gly Lys Ser Lys Ala  
50 55 60  
Lys Ile Gly Asn Asp Thr Ile Leu Phe Thr Leu Tyr Lys Lys Glu Pro  
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85 90 95  
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Lys Ala Lys  
100 105 110  
Glu Ala Thr Glu Ala Lys Ala Val Ala Lys Arg Glu Asp Gln Arg Tyr  
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Ala Trp Lys Glu Cys Gln Lys Lys Ala Asp Gly Gln Lys Arg Val Gln  
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Arg Lys Glu Lys Pro Leu Glu Gly Lys Gln Ala Glu Glu Thr Lys Ala  
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195 200 205  
Thr Arg Gly Arg Asn Trp Glu Asn Ile Phe Pro Glu Lys Leu Lys Glu  
210 215 220  
Asp Arg Val Pro Ala Pro Arg Ser Ala Gly Ser Ile Gln Ile Ser Phe  
225 230 235 240  
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245 250 255  
Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala Met Ser  
260 265 270  
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275 280 285  
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290 295 300

Leu Ala Ala Val Asp Ala Tyr Asn Leu Ala Ile Arg Leu Asn Cys Lys  
 305 310 315 320  
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 Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu Gly Leu  
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Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp		
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gtg ttc tgc atg gaa aac tat ctg aag gtc aac ttt cct cca ttt tta		144
Val Phe Cys Met Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu		
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ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca		192
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala		
50                   55                   60		
aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg		240
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala		
65                   70                   75                   80		
gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag atg atg		288
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met		
85                   90                   95		
caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa		336
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys		
100                105                110		
gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat		384
Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr		
115                120                125		
gca cta agt gtc atg atg aag att gaa gaa gaa gag agg aaa aaa ata		432
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Arg Lys Lys Ile		
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gcc tgg aaa gaa tat caa aga aaa gct gag gag caa aaa aaa att cag Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln 165 170 175	528
aga gaa gag aaa tta tgt caa aaa gaa aag caa att aaa gaa gaa aga Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg 180 185 190	576
aaa aaa ata aaa tat aag agt ctt act aga aat ttg gca tct aga aat Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn 195 200 205	624
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aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att aaa atc Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile 225 230 235 240	720
aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca caa gta Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val 245 250 255	768
gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga aga gca Ala Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala 260 265 270	816
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aac cca gaa tgg ttg aag gat aaa gga aac aaa ttg ttt gca aca gaa Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu 290 295 300	912
aac tat ttg gca gct atc aat gca tat aat tta gcc ata aga cta aat Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn 305 310 315 320	960
aat aag atg cca cta ttg tat ttg aac cgg gct gct tgc cac cta aaa Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys 325 330 335	1008
cta aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu 340 345 350	1056
tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala 355 360 365	1104
cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu 370 375 380	1152

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Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr			
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Val Phe Cys Met Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu			
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Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala			
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Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala			
65	70	75	80
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met			
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Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys			
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Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr			
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Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Arg Lys Lys Ile			
130	135	140	
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu			
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Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln			
165	170	175	
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg			
180	185	190	
Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn			
195	200	205	
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu			
210	215	220	

Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile  
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 245 250 255  
 Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala  
 260 265 270  
 Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys  
 275 280 285  
 Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu  
 290 295 300  
 Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn  
 305 310 315 320  
 Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys  
 325 330 335  
 Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu  
 340 345 350  
 Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala  
 355 360 365  
 His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu  
 370 375 380  
 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys  
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 405 410 415  
 Glu Leu Lys Ser  
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 Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp  
 20 25 30  
  
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 Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu

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		60	
aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala	65	70	240
		75	80
gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag atg atg Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met	85	90	288
		95	
caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys	100	105	336
		110	
gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr	115	120	384
		125	
gca cta agt gtc atg atg aag att gaa gaa gag agg aaa aaa ata Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Arg Lys Lys Ile	130	135	432
		140	
gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gaa ttg gaa Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu	145	150	480
		155	160
gcc tgg aaa gaa tat caa aga aaa gct gag gag caa aaa gaa att cag Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Glu Ile Gln	165	170	528
		175	
aga gaa gag aag tta tgt caa aaa gaa aag caa att aaa gaa gaa aga Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg	180	185	576
		190	
aaa aaa tta aaa tat aag agt ctt act aga aat ttg gca tct aga aat Lys Lys Leu Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn	195	200	624
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ctt gct cca aaa ggg aga aat tca gaa aat ata ttt act gag aag tta Leu Ala Pro Lys Glu Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu	210	215	672
		220	
aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att aaa atc Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile	225	230	720
		235	240
aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca caa gta Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val	245	250	768
		255	
gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga aga gca Ala Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala	260	265	816
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atg aat act gac ata gct gaa ctt tgc gat tta aaa gaa gaa gaa aag Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Lys	275	280	864
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aac cca gaa tgg ttg aag gat aaa gga aac aaa ttg ttt gca aca gaa Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu 290 295 300	912
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aat aag atg cca cta ttg tat ttg aac cg <sup>g</sup> gct gtc cac cta aaa Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys 325 330 335	1008
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 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys  
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 65 70 75 80  
  
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 Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Thr Met  
 85 90 95  
  
 caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa 336  
 Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys  
 100 105 110  
  
 gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat 384  
 Glu Ala Thr Glu Ala Ala Lys Arg Glu Asp Gln Lys Tyr  
 115 120 125  
  
 gca cta agt gtc atg atg aag att gaa gaa gag agg aaa aaa ata 432  
 Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Arg Lys Lys Ile  
 130 135 140  
  
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 Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu  
 145 150 155 160  
  
 gcc tgg aaa gaa tat caa aga aaa gct gag gag cac aaa aaa att cag 528  
 Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu His Lys Lys Ile Gln  
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180	185	190	
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ctt gct cca aaa gga aga aat tca gaa aat ata ttt act gag aag tta Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu 210	215	220	672
aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att aaa atc Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile 225	230	235	720
aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca caa gta Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val 245	250	255	768
gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga aga gca Ala Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala 260	265	270	816
atg aat act gac ata gct gaa ctt tgc gat tta aaa gaa gaa gaa aag Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys 275	280	285	864
aac cca gaa tgg ttg aag gat aaa gga aac aaa ttg ttt gca aca gaa Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu 290	295	300	912
aac tat ttg gca gct atc aat gca tat aat tta gcc ata aga cta aat Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn 305	310	315	960
aat aag atg cca cta ttg tat ttg aac cg <sup>g</sup> gct gct tgc cac cta aaa Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys 325	330	335	1008
cta aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu 340	345	350	1056
tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala 355	360	365	1104
cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu 370	375	380	1152
ggc cta cag gat tat gaa gc <sup>g</sup> gca ctt aag att gat cca tcc aac aaa Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys 385	390	395	1200
att gta caa att gat gct gag aag att cg <sup>g</sup> aat gta att caa gga aca Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr 405	410	415	1248
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Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu  
35                 40                 45  
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala  
50                 55                 60  
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala  
65                 70                 75                 80  
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Thr Met  
85                 90                 95  
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys  
100               105               110  
Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr  
115               120               125  
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Arg Lys Lys Ile  
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Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu  
145               150               155               160  
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu His Lys Lys Ile Gln  
165               170               175  
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg  
180               185               190  
Lys Lys Leu Lys Tyr Lys Ser Leu Thr Arg Asn Ser Ala Ser Arg Asn  
195               200               205  
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu  
210               215               220  
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile  
225               230               235               240  
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val  
245               250               255  
Ala Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala  
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gtc ttt ctg tct ctg ccc ctc aaa ggc gtg tgc gtc aga gac acg gac      96
Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp
20                     25                         30
gtg ttc tgc acg gaa aac tat ctg aag gtc aac ttt cct cca ttt tta      144
Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu
35                     40                         45
ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca      192
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala
50                     55                         60
aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg      240
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala
65                     70                         75                         80
gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag atg atg      288

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Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met			
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caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa			336
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys			
100	105	110	
gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat			384
Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr			
115	120	125	
gca cta agt gtc atg atg aag att gaa gaa gag agg aaa aaa ata			432
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Arg Lys Lys Ile			
130	135	140	
gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gaa ttg gaa			480
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu			
145	150	155	160
gcc tgg aaa gaa tat caa aga aaa gct gag gag caa aaa aaa att cag			528
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln			
165	170	175	
aga gaa gag aaa tta tgt caa aaa gaa aag caa att aaa gaa gaa aga			576
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg			
180	185	190	
aaa aaa ata aaa tat aag agt ctt act aga aat ttg gca tct aga aat			624
Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn			
195	200	205	
ctt gct cca aaa ggg aga aat tca gaa aat ata ttt act gag aag tta			672
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210	215	220	
aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att aaa atc			720
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile			
225	230	235	240
aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca caa gta			768
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val			
245	250	255	
gca gaa gag gag tgg ctg cac aaa caa gct gag gca cga aga gca			816
Ala Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala			
260	265	270	
atg aat act gac ata gct gaa ctt tgc gat tta aaa gaa gaa aag			864
Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys			
275	280	285	
aac cca gaa tgg ttg aag gat aaa gga aac aaa ttg ttt gca aca gaa			912
Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu			
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Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn			
305	310	315	320
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Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys			

325	330	335	
ctt aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu 340	345	350	1056
tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala 355	360	365	1104
cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu 370	375	380	1152
ggc cta cag gat tat gaa gcg gca ctt aag att gat cca tcc aac aaa Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys 385	390	395	1200
att gta caa att gat gct gag aag att cggt aat gta att caa gga aca Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr 405	410	415	1248
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Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala 65 70 75 80			
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Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys 100 105 110			
Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr 115 120 125			
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Arg Lys Lys Ile 130 135 140			
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu			

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Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln			
165                            170                            175			
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg			
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Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn			
195                            200                            205			
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu			
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Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile			
225                            230                            235                            240			
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val			
245                            250                            255			
Ala Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala			
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Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Lys			
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Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu			
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Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu			
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His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu			
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385                            390                            395                            400			
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